CLAIMS AS AMENDED SEPTEMBER 25, 2002

22. (New) A method of analyzing nucleotide sequence of a polynucleotide of interest, comprising;

a) (1) attaching at least one array of one or more sets of consecutive oligonucleotides having known sequences of N nucleotides in length, wherein each oligonucleotide primer differs from the others in the set by one base at the 3' end, to a solid support at known locations; or
(2) providing at least one array of one or more sets of consecutive oligonucleotides having known sequences of N nucleotides in length, wherein each oligonucleotide primer differs from the others in the set by one base at the 3' end, wherein said array is attached to a solid support at known locations;

b) incubating said array of oligonucleotides in the presence of Sequenase® Version 2.0, the polynucleotide of interest, and at least one terminating nucleotide, to generate annealed primers, such that the annealed primers are extended by polymerase-mediated addition of a single terminating nucleotide;

c) identifying the incorporated terminating nucleotide at each array position at which a terminating nucleotide has been incorporated ; and

d) determining the nucleotide sequence of the polynucleotide of interest from the identification of the incorporated nucleotide and the sequence of the oligonucleotide at each array position at which a terminating nucleotide has been incorporated.

23. (New) The method of Claim 22, wherein each array position contains an oligonucleotide primer capable of hybridizing to said polynucleotide of interest.

24. (New) The method of Claim 22, wherein said array of sets of oligonucleotide primers contains all permutations of nucleotides for oligonucleotides of the specified size.

25. (New) The method of Claim 22, wherein said array of sets of oligonucleotide primers comprises oligonucleotides of all possible permutations of N-mers where N is from about 7 to about 30 nucleotides.

26. (New) The method of Claim 22, wherein said method is conducted in the presence of dideoxy guanine, dideoxy adenine, dideoxy threonine and dideoxy cytosine, wherein at least one of said dideoxy nucleotides is fluorescently labeled.

27. (New) The method of Claim 26, wherein each of said dideoxy nucleotides is fluorescently labeled, such that each dideoxy nucleotide is labeled with a different color.

28. (New) The method of Claim 22, wherein said polynucleotide of interest comprises DNA.

29. (New) The method of Claim 22, wherein said polynucleotide of interest comprises RNA.

30. (New) The method of Claim 22, further comprising analyzing the nucleotide sequence of the polynucleotide of interest and of a complement of the polynucleotide of interest.

31. (New) The method of Claim 26, wherein the DNA comprises a gene or portion thereof associated with a heritable disease.

32. (New) The method of Claim 31, wherein said gene or portion thereof is analyzed for an alteration associated with said heritable disease.

33. (New) The method of Claim 32, wherein said heritable disease is cystic fibrosis.

34. (New) The method of Claim 26, wherein the DNA comprises a gene or portion thereof wherein said gene or portion thereof is associated with a heritable disease selected from the group consisting of: cystic fibrosis, β-thalassemia, α-1, Gaucher's Disease, Tay Sach's Disease, and Lesch-Nyham Syndrome.

35. (New) The method of Claim 22, wherein the oligonucleotide primers are immobilized on a solid support.

36. (New) The method of Claim 35, wherein said support is selected from the group consisting of glass and silicon.

37. (New) The method of Claim 22, wherein said oligonucleotide primers comprise fewer than all permutations of nucleotides for oligonucleotides of a specified size.

38. (New) The method of Claim 22, wherein the single base extension is conducted in the presence of nucleotides, wherein the nucleotides consist of terminating nucleotides.

39. (New) A method of analyzing nucleotide sequence of a polynucleotide of interest, comprising;

a) (1) attaching at least one array of one or more sets of consecutive oligonucleotides having known sequences of N nucleotides in length, wherein each oligonucleotide primer differs from the others in the set by one base at the 3' end, to a solid support at known locations; or
(2) providing at least one array of one or more sets of consecutive oligonucleotides having known sequences of N nucleotides in length, wherein each oligonucleotide primer differs from the others in the set by one base at the 3' end, wherein said array is attached to a solid support at known locations;

b) incubating said array of oligonucleotides in the presence of T7 DNA polymerase, the polynucleotide of interest, and at least one terminating nucleotide, to generate annealed primers, such that non-hybridized 3' terminal nucleotides of the annealed primers are removed by the T7 DNA polymerase, and such that the annealed primers are extended by T7 DNA polymerase-mediated addition of a single terminating nucleotide;

c) identifying the incorporated terminating nucleotide at each array position at which a terminating nucleotide has been incorporated; and

d) determining the nucleotide sequence of the polynucleotide of interest from the identification of the incorporated nucleotide and the sequence of the oligonucleotide at each array position at which a terminating nucleotide has been incorporated.

40. (New) The method of Claim 39, wherein each array position contains an oligonucleotide primer capable of hybridizing to said polynucleotide of interest.

41. (New) The method of Claim 39, wherein said array of sets of oligonucleotide primers contains all permutations of nucleotides for oligonucleotides of the specified size.

42. (New) The method of Claim 39, wherein said array of sets of oligonucleotide primers comprises oligonucleotides of all possible permutations of N-mers where N is from about 7 to about 30 nucleotides.

43. (New) The method of Claim 39, wherein said method is conducted in the presence of dideoxy guanine, dideoxy adenine, dideoxy threonine and dideoxy cytosine, wherein at least one of said dideoxy nucleotides is fluorescently labeled.

44. (New) The method of Claim 43, wherein each of said dideoxy nucleotides is fluorescently labeled, such that each dideoxy nucleotide is labeled with a different color.

45. (New) The method of Claim 39, wherein said polynucleotide of interest comprises DNA.

46. (New) The method of Claim 39, wherein said polynucleotide of interest comprises RNA.

47. (New) The method of Claim 39, further comprising analyzing the nucleotide sequence of the polynucleotide of interest and of a complement of the polynucleotide of interest.

48. (New) The method of Claim 45, wherein the DNA comprises a gene or portion thereof associated with a heritable disease.

49. (New) The method of Claim 48, wherein said gene or portion thereof is analyzed for an alteration associated with disease.

50. (New) The method of claim 49, wherein said disease is cystic fibrosis.

51. (New) The method of Claim 45, wherein the DNA comprises a gene or portion thereof wherein said gene or portion thereof is associated with a heritable disease selected from the group consisting of: cystic fibrosis, β-thalassemia, α-1, Gaucher's Disease, Tay Sach's Disease, and Lesch-Nyham Syndrome.

52. (New) The method of Claim 39, wherein the oligonucleotide primers are immobilized on a solid support.

53. (New) The method of Claim 52, wherein said support is selected from the group consisting of glass and silicon.

54. (New) The method of Claim 39, wherein said oligonucleotide primers comprise fewer than all permutations of nucleotides for oligonucleotides of a specified size.

55. (New) The method of Claim 39, wherein the single base extension is conducted in the presence of nucleotides, wherein the nucleotides consist of terminating nucleotides.

56. (New) A kit for determining nucleotide sequence of a polynucleotide of interest, comprising an array of oligonucleotide primers, immobilized on a solid support at known locations wherein each location contains a unique oligonucleotide primer, T7 DNA polymerase, and at least one terminating oligonucleotide.

57. (New) The kit of Claim 56, further comprising Sequenase® Version 2.0.

58. (New) The kit of Claim 56, wherein the terminating nucleotides are labeled, such that each labeled terminating nucleotide can be distinguished from the other labeled terminating nucleotides.